

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 219.37 Seconds  
(without alignments)  
4337.914 Million cell updates/sec

Title: US-09-943-115A-8

Perfect score: 25

Sequence: 1 tcttaggtcttctccaccacaaat 25

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gssi.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	87.2	810	6	CB339857
2	20.2	80.8	626	8	AZ307169
3	19.8	79.2	455	6	CB741675
4	19.8	79.2	673	8	BZ803457
5	19.8	79.2	843	9	CG183873
6	19.4	77.6	556	8	CQ062244
7	19.4	77.6	987	5	BQ956803
8	19.2	76.8	941	7	CO020587
9	18.8	75.2	518	8	AZ808593
10	18.6	74.4	182	2	BE223371
11	18.6	74.4	344	7	CO939972
12	18.6	74.4	349	5	BX914384
13	18.6	74.4	430	5	BX882094
14	18.6	74.4	472	8	BH275616
15	18.6	74.4	531	2	AV971360
16	18.6	74.4	543	1	AL588321
17	18.6	74.4	545	2	AV983945
18	18.6	74.4	549	4	BG710511
19	18.6	74.4	551	5	BW042006
20	18.6	74.4	565	1	AJ398343
21	18.6	74.4	577	8	AZ958073
22	18.6	74.4	604	4	BI065397
23	18.6	74.4	604	5	BW078263
24	18.6	74.4	616	9	AG239252

25	18.6	74.4	625	4	BI065075
26	18.6	74.4	641	5	BW043881
27	18.6	74.4	643	4	EG713114
28	18.6	74.4	652	7	CK726252
29	18.6	74.4	676	1	AA702791
30	18.6	74.4	686	5	BW448117
31	18.6	74.4	690	5	BW090595
32	18.6	74.4	698	5	BW077639
33	18.6	74.4	702	5	BW033237
34	18.6	74.4	730	5	BW429347
35	18.6	74.4	750	9	CL014894
36	18.6	74.4	759	6	CB991210
37	18.6	74.4	762	8	AQ747999
38	18.6	74.4	768	7	CO983347
39	18.6	74.4	775	6	CB990421
40	18.6	74.4	786	5	BX871836
41	18.6	74.4	805	9	CC595391
42	18.6	74.4	808	6	CA512261
43	18.6	74.4	815	6	CB991778
44	18.6	74.4	835	7	CN321869
45	18.6	74.4	837	7	CN331567

## ALIGNMENTS

CB339857 810 bp mRNA linear EST 14-MAR-2003  
CA23EI02IVRB\_G02 Cabernet Sauvignon Leaf - CA23EI Vitis vinifera  
cDNA clone CA23EI02IVRB\_G02 3', mRNA sequence.

CB339857  
EST  
CB339857.1 GI:28959713

Vitis vinifera

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; Vitaceae; Vitis.

1 (bases 1 to 810)

Jones da Silva, F., Lim, H., Iandolino, A., Baek, J., Leslie, A., Xu, J.,

Gomes, K., Walker, M.A., and Cook, D.R.

Transcriptional responses of Vitis vinifera to infection by the

bacterial pathogen Xylella fastidiosa

Unpublished (2003)

Contact: Douglas Cook, PhD

CAES Genome Facility

UC Davis, Plant Pathology

One Shields Ave, Davis, CA 95616, USA

Tel: 530 754 6561

Fax: 530 754 6617

Email: drock@ucdavis.edu

Seq primer: GCCAACGATGCTGCTAG.

Location/Qualifiers

1..810

/organism="Vitis vinifera"

/mol\_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db\_xref="taxon:29760"

/clone="CA23EI02IVRB\_G02"

/sex="Hermaphrodite"

/dev\_stage="Mid-season leaf material, collected July 25,

2001."

/lab\_host="DHSalpha"

/clone\_lib="Cabernet Sauvignon Leaf - CA23EI"

/note="Organ: Leaf; Vector: pDNR; Site: Sfil; Site: 2;

Sfil; CA23EI is a cDNA library of Cabernet Sauvignon

leaves. The leaves were collected on July 25, 2001, in

Napa Valley, California, and represent leaves in

mid-season development. These leaves were verified to be

infected with the bacterial pathogen, Xylella fastidiosa,

based on a diagnostic assay using PCR and Xylella-specific

primer pairs. The plants were asymptomatic at the time of

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 140.652 Seconds  
(without alignments)  
1103.355 Million cell updates/sec

Title: US-09-943-115A-8  
Perfect score: 25  
Sequence: 1 tcttagagctcttctcaccacaaact 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
23: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
24: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
25: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
27: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	10	US-09-943-115A-8
C 2	25	100.0	1345	10	US-09-943-115A-1
C 3	25	100.0	1345	14	US-10-146-575-3
C 4	25	100.0	1345	14	US-10-085-612-3
C 5	25	100.0	12983	21	US-10-415-607-1
C 6	25	100.0	13035	15	US-10-121-960C-14
C 7	25	100.0	15185	15	US-10-121-960C-17
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 14, Appli
					Sequence 17, Appli

C 8	25	100.0	96960	21	US-10-484-577-662	Sequence 662, App
C 9	22.4	89.6	1012	9	US-09-957-997-4	Sequence 4, Appli
C 10	22.4	89.6	11186	9	US-09-957-997-1	Sequence 1, Appli
C 11	22.4	89.6	11186	21	US-10-415-607-4	Sequence 4, Appli
C 12	19.2	76.8	8943	17	US-10-257-166-47	Sequence 47, Appli
C 13	18.8	75.2	8205	9	US-09-860-670-276	Sequence 276, App
C 14	18.8	75.2	8205	17	US-10-227-646-276	Sequence 276, App
C 15	18.8	75.2	2666	13	US-10-087-192-1777	Sequence 1777, App
C 16	18.8	75.2	28446	19	US-10-331-053-13	Sequence 13, Appli
C 17	18.8	75.2	100685	19	US-10-388-838-93	Sequence 93, Appli
C 18	18.6	74.4	541	13	US-10-027-632-91527	Sequence 91527, A
C 19	18.6	74.4	541	13	US-10-027-632-307501	Sequence 307501, A
C 20	18.6	74.4	541	17	US-10-027-632-91527	Sequence 91527, A
C 21	18.6	74.4	541	17	US-10-027-632-307501	Sequence 307501, A
C 22	18.6	74.4	1254	14	US-10-085-612-4	Sequence 4, Appli
C 23	18.4	73.6	1223197	13	US-10-027-632-179264	Sequence 179264, A
C 24	18.4	73.6	1223197	17	US-10-027-632-179264	Sequence 179264, A
C 25	18.2	72.8	508	9	US-09-878-178-2224	Sequence 2224, App
C 26	18.2	72.8	508	13	US-10-046-935-2224	Sequence 2224, App
C 27	18.2	72.8	508	14	US-10-146-502-2224	Sequence 2224, App
C 28	18.2	72.8	589	21	US-10-487-901-1682	Sequence 1682, App
C 29	18.2	72.8	633	13	US-10-027-632-255622	Sequence 255622, A
C 30	18.2	72.8	633	17	US-10-027-632-255622	Sequence 255622, A
C 31	18.2	72.8	637	13	US-10-027-632-188102	Sequence 188102, A
C 32	18.2	72.8	637	17	US-10-027-632-188102	Sequence 188102, A
C 33	18.2	72.8	4145	20	US-10-335-053-230	Sequence 230, App
C 34	18.2	72.8	104729	20	US-10-723-860-1434	Sequence 1434, App
C 35	17.8	71.2	559	13	US-10-027-632-231930	Sequence 231930, A
C 36	17.6	70.4	337	21	US-10-027-632-231930	Sequence 231930, A
C 37	17.6	70.4	337	21	US-10-914-037-898	Sequence 898, App
C 38	17.6	70.4	437	9	US-09-878-178-1397	Sequence 1397, App
C 39	17.6	70.4	437	13	US-10-046-935-1397	Sequence 1397, App
C 40	17.6	70.4	437	14	US-10-146-502-1397	Sequence 1397, App
C 41	17.6	70.4	558	19	US-10-437-963-200	Sequence 200, App
C 42	17.6	70.4	685	13	US-10-027-632-199874	Sequence 199874, A
C 43	17.6	70.4	685	17	US-10-027-632-199874	Sequence 199874, A
C 44	17.6	70.4	1086	10	US-09-814-353-19227	Sequence 19227, A
C 45	17.6	70.4	1391	9	US-09-969-708-480	Sequence 480, App

## ALIGNMENTS

RESULT 1  
US-09-943-115A-8  
; Sequence 8, Application US/09943115A  
; Publication No. US20030017469A1  
; GENERAL INFORMATION:  
; APPLICANT: SEQUENOM, Inc.  
; APPLICANT: Risinger, Carl  
; APPLICANT: Andersson, Maria  
; APPLICANT: Lewander, Tommy  
; APPLICANT: Olafsson, Erik  
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9  
; TITLE OF INVENTION: POLYMORPHISMS  
; FILE REFERENCE: 52459-20021.00  
; CURRENT APPLICATION NUMBER: US/09/943,115A  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: UK 0021286.0  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-943-115A-8

Query Match 100.0%; Score 25; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:12:33 ; Search time 24.8229 Seconds  
(without alignments)  
5961.965 Million cell updates/sec

Title: US-09-943-115a-8

Perfect score: 25

Sequence: 1 tcttagagctcttctcaccacaaact 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001s:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002s:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003s:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004s:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	6	ABK68752 PCR prime
C 2	25	100.0	1345	2	Aax28296 Human CYP
C 3	25	100.0	1345	3	Aax57019 Nucleic a
C 4	25	100.0	1345	3	Aax57020 Nucleic a
C 5	25	100.0	1345	6	ABK68745
C 6	25	100.0	1345	12	ADJ84441 Human phe
C 7	25	100.0	12983	13	ADJ84441 Human CYP
C 8	25	100.0	12983	6	ADJ84441 Human CYP
C 9	25	100.0	13035	8	ADJ84441 Human CYP
C 10	25	100.0	13185	8	ADJ84441 Human CYP
C 11	25	100.0	39071	12	ADM97420 Prostate
C 12	25	100.0	96960	8	ACF62734 Cancer ba
C 13	25	100.0	96960	8	ACF62734 Cancer ba
C 14	25	100.0	96960	10	ADB87938 Human UGT
C 15	25	100.0	96960	10	ADB87938 Human UGT
C 16	25	100.0	96960	10	ADB87938 Human UGT
C 17	25	100.0	123785	10	ABX77171 DNA sequ
C 18	22.4	89.6	1012	6	AD36215 Human pro
C 19	22.4	89.6	11186	6	AD41242 Human CYP
C 20	22.4	89.6	11186	6	AD436213 Human cyt

ALIGNMENTS

RESULT 1

ABK68752

ID ABK68752 standard; DNA; 25 BP.

XX AC ABK68752;

XX DT 02-JUL-2002 (first entry)

XX DE PCR primer #2 for detecting SNP in 5'-region of human CYP3A4 gene.

XX KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;

XX RW PCR; primer; ss.

XX OS Homo sapiens.

XX PN WO200218641-A2.

XX PD 07-MAR-2002.

XX PF 30-AUG-2001; 2001WO-IB001580.

XX PR 30-AUG-2000; 2000GB-00021286.

XX PA (GEMI-) GEMINI GENOMICS PLC.

XX PI Risinger C, Andersson MK, Lewander T, Olaisson E;

XX DR WPI; 2002-351712/38.

XX PT Novel primer pairs and sequence determination oligonucleotides useful for

XX PT amplifying and detecting novel single nucleotide polymorphisms in the 5'

XX PT flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes

XX PS Claim 2; Page 15; 47pp; English.

XX CC The present invention relates to PCR primer pairs for amplifying and

XX CC sequence determination oligonucleotides for detecting single nucleotide

XX CC polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450

XX CC (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position

XX CC 461 of a defined 1345 base pair sequence for CYP3A4 or position 957

XX CC 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.

XX CC The PCR primers are useful for amplifying the CYP sequences and the

Ad89689 Oligonucle  
Ad89415 Oligonucle  
Abk3966 Human che  
Aak90749 Human dig  
Aai62948 Human gen  
Acn45032 Mouse gen  
Abd32735 Mouse can  
Abk39410 Human CYP  
Abk39524 Human CYP  
Abk39501 Human CYP  
Abk39411 Human CYP  
Abk39409 Human CYP  
Abk39499 Human CYP  
Abk39500 Human CYP  
Abk39412 Human CYP  
Aas51756 Cytochrom  
Ab138635 Human col  
Adk54299 Plant DNA  
Adi17894 DNA (Seqi  
Add16076 Human alb  
Add29781 Human tum  
Adq18615 Human eof  
Ab137808 Human col  
Abn62332 Human can

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:18:28 ; Search time 127.727 Seconds  
(without alignments)  
9484.165 Million cell updates/sec

Title: US-09-943-115A-8

Perfect score: 25  
Sequence: 1 tcttagagttcttctcaccacaaact 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	25	100.0	25	6	AX421260	AX421260 Sequence
C 2	25	100.0	1013	9	AF181105	AF181105 Homo sapi
C 3	25	100.0	1345	6	AR142139	AR142139 Sequence
C 4	25	100.0	1345	6	AR142140	AR142140 Sequence
C 5	25	100.0	1345	6	BD222974	BD222974 CYP3A4 NF
C 6	25	100.0	1345	6	BD222975	BD222975 CYP3A4 NF
C 7	25	100.0	1345	6	CQ776018	CQ776018 Sequence
C 8	25	100.0	1345	6	CQ790615	CQ790615 Sequence
C 9	25	100.0	1345	6	AR222893	AR222893 Sequence
C 10	25	100.0	1345	6	AX421253	AX421253 Sequence
C 11	25	100.0	1345	9	HUMCYP3A4	D1131 Homo sapien
C 12	25	100.0	6101	6	CQ806643	CQ806643 Sequence
C 13	25	100.0	11374	9	AF185589	AF185589 Homo sapi
C 14	25	100.0	96960	6	AX706964	AX706964 Sequence
C 15	25	100.0	96960	6	AX707894	AX707894 Sequence
C 16	25	100.0	123778	9	AC069294	AC069294 Homo sapi
C 17	25	100.0	170470	9	AC146392	AC146392 Pan trogl
C 18	25	100.0	174832	9	AF280107	AF280107 Homo sapi
C 19	23.4	93.6	173861	2	AC141417	AC141417 Papio anu

C 20	23.4	93.6	183854	2	AC145951	AC145951 Pan trogl
C 21	22.4	89.6	1012	9	AF181861	AF181861 Homo sapi
C 22	22.4	89.6	11186	9	AF329900	AF329900 Homo sapi
C 23	21.8	87.2	6101	6	CQ806981	CQ806981 Sequence
C 24	21.8	87.2	6101	6	CQ807255	CQ807255 Sequence
C 25	20.4	81.6	190317	2	AC137848	AC137848 Mus muscu
C 26	20.2	80.8	121190	2	AC151659	AC151659 Dasyypus n
C 27	20.2	80.8	143723	2	AC101763	AC101763 Mus muscu
C 28	20.2	80.8	235733	2	AC114859	AC114859 Rattus no
C 29	20.2	80.8	235739	2	AC121421	AC121421 Rattus no
C 30	19.8	79.2	42566	2	AC149313	AC149313 Phakophor
C 31	19.8	79.2	165235	10	AC145398	AC145398 Rattus no
C 32	19.8	79.2	192707	2	AC116250	AC116250 Rattus no
C 33	19.8	79.2	195798	2	AC118890	AC118890 Rattus no
C 34	19.8	79.2	252721	2	AC095946	AC095946 Rattus no
C 35	19.4	77.6	110000	2	AC073157	AC073157 Homo sapi
C 36	19.4	77.6	115984	9	HS292F10	HS292F10 Human DNA
C 37	19.4	77.6	120664	9	AP000887	AP000887 Homo sapi
C 38	19.4	77.6	163999	2	AC141207	AC141207 Rattus no
C 39	19.4	77.6	167398	9	AC069227	AC069227 Homo sapi
C 40	19.4	77.6	171266	9	AF404777	AF404777 Homo sapi
C 41	19.4	77.6	226406	2	AC095975	AC095975 Rattus no
C 42	19.4	77.6	234457	2	AC109698	AC109698 Rattus no
C 43	19.4	77.6	234597	2	AC127638	AC127638 Rattus no
C 44	19.4	77.6	257605	2	AC120627	AC120627 Rattus no
C 45	19.4	77.6	267829	2	AC120979	AC120979 Rattus no

## ALIGNMENTS

RESULT 1  
AX421260  
LOCUS AX421260  
DEFINITION Sequence 8 from Patent WO218641.  
ACCESSION AX421260  
VERSION AX421260.1 GI:21524668  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Olaisson,E.  
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms  
JOURNAL Patent: WO 0218641-A 8 07-MAR-2002;  
FEATURES  
Gemini Genomics PLC (GB)  
Location/Qualifiers  
1..25  
/organism="synthetic construct"  
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/note="Primer"

ORIGIN  
Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTTAGAGTCTTCTCTCACCACAACT 25  
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DB 1 TCTTAGAGTCTTCTCTCACCACAACT 25

RESULT 2  
AF181105/c  
LOCUS AF181105  
DEFINITION Homo sapiens cytochrome P-45011A4 (CYP3A4) gene, promoter region.  
ACCESSION AF181105  
VERSION AF181105.1 GI:5853303  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 175.496 Seconds  
(without alignments)  
4337.914 Million cell updates/sec

Title: us-09-943-115a-7  
Perfect score: 20  
Sequence: 1 ccagcctgaagtgcagaga 20  
Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST:  
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2: gb\_est2:  
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5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	19	95.0	533	2	BE400241	BE400241 AMB001.A0
4	19	95.0	553	4	BG039424	BG039424 NXSI_098
5	19	95.0	565	6	CD923330	CD923330 G750.107N
6	19	95.0	636	6	CD936872	CD936872 OV.105F13
7	17.4	87.0	203	7	CV330241	CV330241 IL2-UT007
8	17.4	87.0	325	2	BE776859	BE776859 MY-21-E-0
9	17.4	87.0	346	9	CE095752	CE095752 tigr-gss
10	17.4	87.0	404	1	AA729069	AA729069 mw03a09.s
11	17.4	87.0	409	5	BA482078	BA482078 DKFZp686N
12	17.4	87.0	569	5	BX920785	BX920785 BX920785
13	17.4	87.0	572	7	H98072	H98072 vx06d02.sl
14	17.4	87.0	598	1	A1686927	A1686927 tp91d05.x
15	17.4	87.0	622	8	AZ967380	AZ967380 2M0238KL3
16	17.4	87.0	631	9	CE703536	CE703536 tigr-gss
17	17.4	87.0	652	1	A1445869	A1445869 t12g12.x
18	17.4	87.0	729	6	CA345627	CA345627 676319 NC
19	17.4	87.0	749	6	CA348148	CA348148 679395 NC
20	17	85.0	437	4	BJ682390	BJ682390 BJ682390
21	17	85.0	443	4	BI063793	BI063793 IL3-UT011
22	17	85.0	461	7	CV419454	CV419454 RC4-C1019
23	17	85.0	476	4	BI397594	BI397594 NXPV 101
24	17	85.0	498	4	BG832753	BG832753 NXPV_079

25	17	85.0	615	1	AJ737738	AJ737738 AJ737738
26	17	85.0	665	5	BU212860	BU212860 604153436
27	17	85.0	691	4	BJ685677	BJ685677 BJ685677
28	17	85.0	694	4	BJ676309	BJ676309 BJ676309
29	17	85.0	696	1	AJ737746	AJ737746 AJ737746
30	17	85.0	794	5	BU239104	BU239104 603323633
31	17	85.0	818	5	BU226227	BU226227 603948862
32	17	85.0	833	5	BU248598	BU248598 603591241
33	16.8	84.0	228	2	BB227240	BB227240 BB227240
34	16.8	84.0	344	4	BI317060	BI317060 saf84c02
35	16.8	84.0	349	8	BZ848825	BZ848825 CH240_240
36	16.8	84.0	403	6	CB812370	CB812370 AMGNNUC:S
37	16.8	84.0	430	4	BI941950	BI941950 8611109.Y
38	16.8	84.0	434	4	BG306587	BG306587 fm16b01.Y
39	16.8	84.0	462	1	AA645349	AA645349 v87905.Y
40	16.8	84.0	476	1	A1592418	A1592418 v87905.Y
41	16.8	84.0	483	5	BQ593608	BQ593608 E012766-0
42	16.8	84.0	494	5	BM894646	BM894646 1h69609.Y
43	16.8	84.0	505	1	AL926007	AL926007 AL926007
44	16.8	84.0	505	8	AQ833973	AQ833973 HS 5261.A
45	16.8	84.0	515	8	AQ970303	AQ970303 RFCI-23-3

ALIGNMENTS

RESULT 1  
LOCUS CA637269 511 bp mRNA linear EST 23-NOV-2002  
DEFINITION wrel.pk0002.a5 wrel Triticum aestivum cDNA clone wrel.pk0002.a5 5'  
ACCESSION CA637269  
VERSION CA637269.1 GI:25215565  
KEYWORDS EST  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 511)  
AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,  
Miao,G., Caraher,N. and Hanafey,M.K.  
TITLE DuPont Wheat cDNA Sequence  
JOURNAL Unpublished (2002)  
COMMENT Contact: Scott V. Tingey  
Crop Genetics  
E. I. DuPont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA.  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13.  
Location/Qualifiers  
1. 511  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone="wrel.pk0002.a5"  
/tissue\_type="root"  
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/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:  
XhoI; Wheat (Triticum aestivum L.) root; 7 day old  
etiolated seedling"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCAGCCTGAAGTGCAGAG 19  
Db 82 CCAGCCTGAAGTGCAGAG 100

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 112.521 Seconds  
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1103.355 Million cell updates/sec

Title: US-09-943-115A-7

Perfect score: 20

Sequence: 1 ccagctgaagtgcagaga 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
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- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	1345	10	US-09-943-115A-1
3	20	100.0	1345	14	US-10-146-575-3
4	20	100.0	1345	14	US-10-085-612-3
5	20	100.0	12983	21	US-10-415-607-1
6	20	100.0	13035	15	US-10-121-960C-14
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Query Match 100.0%; Score 20; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1  
US-09-943-115A-7  
Sequence 7, Application US/09943115A  
Publication No. US20030017469A1  
GENERAL INFORMATION:  
APPLICANT: SEQUENOM, Inc.  
APPLICANT: Risinger, Carl  
APPLICANT: Andersson, Maria  
APPLICANT: Lewander, Tommy  
APPLICANT: Olafsson, Erik  
TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9  
FILE REFERENCE: 52459-20021.00  
CURRENT APPLICATION NUMBER: US/09/943,115A  
CURRENT FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: UK 0021286.0  
PRIOR FILING DATE: 2000-08-30  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-943-115A-7

Sequence 662, App  
Sequence 239621,  
Sequence 239621,  
Sequence 20604, A  
Sequence 1, Appli  
Sequence 220069,  
Sequence 220069,  
Sequence 162804,  
Sequence 162804,  
Sequence 139509,  
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Sequence 139510,  
Sequence 139510,  
Sequence 8166, Ap  
Sequence 7314, Ap  
Sequence 30396, A  
Sequence 30396, A  
Sequence 100092,  
Sequence 100092,  
Sequence 83842, A  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 45, Appli  
Sequence 1282, Ap  
Sequence 268083,  
Sequence 268084,  
Sequence 268083,  
Sequence 268084,  
Sequence 275, App  
Sequence 1108, Ap  
Sequence 766, App  
Sequence 41529, A  
Sequence 2629, Ap  
Sequence 3, Appli  
Sequence 1, Appli  
Sequence 60248, A  
Sequence 60248, A

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 19:46:29 ; Search time 5.73654 Seconds  
(without alignments)  
5704.747 Million cell updates/sec

Title: US-09-943-115A-7  
Perfect score: 20  
Sequence: 1 ccagcctgaagtgcagaga 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	1345	US-09-372-339-1	Sequence 1, Appli
2	20	100.0	1345	US-09-372-339-2	Sequence 2, Appli
3	20	100.0	1345	US-09-144-367-3	Sequence 3, Appli
4	20	100.0	31197	US-09-949-016-12963	Sequence 12963, A
5	20	100.0	103934	US-09-949-016-14433	Sequence 14433, A
C 6	17.4	87.0	63658	US-09-949-016-13238	Sequence 13238, A
C 7	17.4	87.0	64489	US-09-949-016-11766	Sequence 11766, A
8	17.4	87.0	144158	US-09-949-016-11755	Sequence 11755, A
9	17.4	87.0	144158	US-09-949-016-11755	Sequence 11755, A
10	16.8	84.0	601	US-09-949-016-197921	Sequence 12936, A
11	16.8	84.0	601	US-09-949-016-197921	Sequence 12936, A
12	16.8	84.0	601	US-09-949-016-197922	Sequence 17922, A
13	16.8	84.0	56616	US-09-949-016-197923	Sequence 17923, A
C 14	16.8	84.0	56616	US-09-949-016-12462	Sequence 12462, A
C 15	16.8	84.0	90541	US-09-949-016-17085	Sequence 17085, A
C 16	16.8	84.0	90541	US-09-759-359A-3	Sequence 3, Appli
C 17	16.8	84.0	156651	US-10-207-973-3	Sequence 3, Appli
C 18	16.4	82.0	990	US-09-949-016-17349	Sequence 17349, A
C 19	15.8	79.0	156	US-09-603-208A-71	Sequence 71, Appl
C 20	15.8	79.0	601	US-09-621-976-11838	Sequence 11838, A
C 21	15.8	79.0	601	US-09-949-016-161246	Sequence 161246, A
C 22	15.8	79.0	601	US-09-949-016-175645	Sequence 175645, A
C 23	15.8	79.0	848	US-09-221-017B-443	Sequence 443, Appl
C 24	15.8	79.0	1132	US-08-651-136C-21	Sequence 21, Appl
C 25	15.8	79.0	1132	US-09-229-911A-21	Sequence 21, Appl
C 26	15.8	79.0	5688	US-09-949-016-16734	Sequence 16734, A
27	15.8	79.0	11002	US-09-949-016-17471	Sequence 17471, A
				US-09-949-016-17472	Sequence 17472, A

28	15.8	79.0	11002	4	US-09-949-016-17473	Sequence 17473, A
C 29	15.8	79.0	20721	4	US-09-949-016-16257	Sequence 16257, A
C 30	15.8	79.0	31078	4	US-09-949-016-14435	Sequence 14435, A
C 31	15.8	79.0	44479	4	US-09-949-016-17176	Sequence 17176, A
32	15.4	77.0	601	4	US-09-949-016-19617	Sequence 19617, A
33	15.4	77.0	601	4	US-09-949-016-175699	Sequence 175699, A
34	15.4	77.0	601	4	US-09-949-016-198633	Sequence 198633, A
35	15.4	77.0	601	4	US-09-949-016-198633	Sequence 198633, A
36	15.4	77.0	1964	3	US-09-434-613-2	Sequence 2, Appli
37	15.4	77.0	1964	4	US-09-963-908-2	Sequence 2, Appli
38	15.4	77.0	1985	4	US-09-620-312D-812	Sequence 812, App
C 39	15.4	77.0	7584	4	US-09-949-016-11836	Sequence 11836, A
C 40	15.4	77.0	7585	4	US-09-949-016-16737	Sequence 16737, A
C 41	15.4	77.0	767677	4	US-09-949-016-12147	Sequence 12147, A
C 42	15.4	77.0	767677	4	US-09-949-016-12147	Sequence 12147, A
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44	15.2	76.0	472	4	US-09-513-999C-12258	Sequence 12258, A
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				4	US-09-702-705-1120	Sequence 1120, Ap

ALIGNMENTS

RESULT 1  
US-09-372-339-1  
; Sequence 1, Application US/09372339  
; Patent No. 6174684  
; GENERAL INFORMATION:  
; APPLICANT: Rebbeck, Timothy  
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor  
; FILE REFERENCE: PENN-0695  
; CURRENT APPLICATION NUMBER: US/09/372,339  
; EARLIER FILING DATE: 1999-08-11  
; EARLIER APPLICATION NUMBER: 60/096,586  
; EARLIER FILING DATE: 1998-08-14  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1345  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-372-339-1

Query Match 100.0%; Score 20; DB 3; Length 1345;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGCCTGAAGTGCAGAGA 20  
Db 294 CCAGCCTGAAGTGCAGAGA 313

RESULT 2  
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; Sequence 2, Application US/09372339  
; Patent No. 6174684  
; GENERAL INFORMATION:  
; APPLICANT: Rebbeck, Timothy  
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor  
; FILE REFERENCE: PENN-0695  
; CURRENT APPLICATION NUMBER: US/09/372,339  
; EARLIER FILING DATE: 1999-08-11  
; EARLIER APPLICATION NUMBER: 60/096,586  
; EARLIER FILING DATE: 1998-08-14  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1345  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-372-339-2

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:18:28 ; Search time 102.181 Seconds  
(without alignments)  
9484.165 Million cell updates/sec

Title: US-09-943-115A-7  
Perfect score: 20  
Sequence: 1 ccagcctgaaagtcagaga 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sta.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX421259
2	20	100.0	1001	6	CQ853861 Sequence
3	20	100.0	1013	9	AF181105 Homo sapi
4	20	100.0	1345	6	AF142139 Sequence
5	20	100.0	1345	6	ARI42140 Sequence
6	20	100.0	1345	6	BD222974 CYP3A4 NF
7	20	100.0	1345	6	BD222975 CYP3A4 NF
8	20	100.0	1345	6	CQ776018 Sequence
9	20	100.0	1345	6	CQ790615 Sequence
10	20	100.0	1345	6	AR222893 Sequence
11	20	100.0	1345	6	AX421253 Sequence
12	20	100.0	1345	9	HMCYCP3A4
13	20	100.0	6101	6	CQ806643
14	20	100.0	11374	9	AF185589 Homo sapi
15	20	100.0	96960	6	AX706964 Sequence
16	20	100.0	96960	6	AX707894 Sequence
17	20	100.0	123778	9	AC069294 Homo sapi
18	20	100.0	174832	9	AF280107 Homo sapi
19	19	95.0	79355	2	AC021280 Homo sapi

C	20	19	95.0	155536	2	AC138877	AC138877 Homo sapi
	21	19	95.0	159287	9	AP003694	AP003694 Homo sapi
	22	19	95.0	161474	2	AC013697	AC013697 Homo sapi
	23	19	95.0	175125	9	AC027031	AC027031 Homo sapi
	24	19	95.0	190910	9	CNS01DUX	ALU13372 Human chr
	25	18.4	92.0	170470	9	AC146392	AC146392 Pan trogl
	26	18.4	92.0	173861	2	AC141417	AC141417 Papio anu
	27	18.4	92.0	208452	10	AC127291	AC127291 Mus muscu
	28	18.4	92.0	222506	2	AC120726	AC120726 Rattus no
	29	18.4	92.0	230518	2	AC097416	AC097416 Rattus no
	30	18.4	92.0	231356	2	AC113626	AC113626 Rattus no
	31	18	90.0	198857	9	AC012404	AC012404 Homo sapi
	32	18	90.0	213865	2	AC145972	AC145972 Gallus ga
	33	17.4	87.0	30175	9	AC004778	AC004778 Homo sapi
	34	17.4	87.0	65937	2	AC102820	AC102820 Mus muscu
	35	17.4	87.0	94000	9	AP000562	AP000562 Homo sapi
	36	17.4	87.0	120173	9	AC137630	AC137630 Homo sapi
	37	17.4	87.0	140300	9	AC015550	AC015550 Homo sapi
	38	17.4	87.0	140739	9	AP005432	AP005432 Homo sapi
	39	17.4	87.0	147731	8	AP005112	AP005112 Oryza sat
	40	17.4	87.0	148508	2	AC027795	AC027795 Homo sapi
	41	17.4	87.0	160215	10	AC092531	AC092531 Rattus no
	42	17.4	87.0	163026	2	AC103883	AC103883 Homo sapi
	43	17.4	87.0	163077	9	AC026362	AC026362 Homo sapi
	44	17.4	87.0	163237	10	AC109192	AC109192 Mus muscu
	45	17.4	87.0	166125	2	AC019327	AC019327 Homo sapi

## ALIGNMENTS

RESULT 1	AX421259	AX421259	Sequence 7 from Patent WO0218641.	20 bp	DNA	linear	PAT 18-JUN-2002
LOCUS	AX421259	AX421259	AX421259.1	GI:21524667			
DEFINITION	AX421259	AX421259	AX421259.1	GI:21524667			
ACCESSION	AX421259	AX421259	AX421259.1	GI:21524667			
VERSION	AX421259	AX421259	AX421259.1	GI:21524667			
KEYWORDS	AX421259	AX421259	AX421259.1	GI:21524667			
SOURCE	AX421259	AX421259	AX421259.1	GI:21524667			
ORGANISM	AX421259	AX421259	AX421259.1	GI:21524667			
REFERENCE	AX421259	AX421259	AX421259.1	GI:21524667			
AUTHORS	AX421259	AX421259	AX421259.1	GI:21524667			
TITLE	AX421259	AX421259	AX421259.1	GI:21524667			
JOURNAL	AX421259	AX421259	AX421259.1	GI:21524667			
FEATURES	AX421259	AX421259	AX421259.1	GI:21524667			
source	AX421259	AX421259	AX421259.1	GI:21524667			

ORIGIN	AX421259	AX421259	AX421259.1	GI:21524667			
Query Match	AX421259	AX421259	AX421259.1	GI:21524667			
Best Local Similarity	AX421259	AX421259	AX421259.1	GI:21524667			
Matches	AX421259	AX421259	AX421259.1	GI:21524667			
Conservative	AX421259	AX421259	AX421259.1	GI:21524667			
Mismatches	AX421259	AX421259	AX421259.1	GI:21524667			
Indels	AX421259	AX421259	AX421259.1	GI:21524667			
Gaps	AX421259	AX421259	AX421259.1	GI:21524667			
QY	AX421259	AX421259	AX421259.1	GI:21524667			
Db	AX421259	AX421259	AX421259.1	GI:21524667			
RESULT 2	AX421259	AX421259	AX421259.1	GI:21524667			
LOCUS	AX421259	AX421259	AX421259.1	GI:21524667			
DEFINITION	AX421259	AX421259	AX421259.1	GI:21524667			
ACCESSION	AX421259	AX421259	AX421259.1	GI:21524667			
VERSION	AX421259	AX421259	AX421259.1	GI:21524667			
KEYWORDS	AX421259	AX421259	AX421259.1	GI:21524667			
SOURCE	AX421259	AX421259	AX421259.1	GI:21524667			
ORGANISM	AX421259	AX421259	AX421259.1	GI:21524667			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	AX421259	AX421259	AX421259.1	GI:21524667			



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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:12:33; Search time 19.8584 Seconds  
(without alignments)  
5961.965 Million cell updates/sec

Title: US-09-943-115A-7

Perfect score: 20

Sequence: 1 ccagcctgaaagtcagaga 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1980s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2000s:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	Abk68751 PCR prime
2	20	100.0	201	12	Adm97390 Prostate
3	20	100.0	1001	13	Adq81033 Human phe
4	20	100.0	1345	2	Aax28296 Human CYP
5	20	100.0	1345	3	Aaz57019 Nucleic a
6	20	100.0	1345	3	Aaz57020 Nucleic a
7	20	100.0	1345	6	Abk68745 5'-flanki
8	20	100.0	1345	12	Adj84441 Human phe
9	20	100.0	6101	13	AdS89077
10	20	100.0	12983	6	AdS89077 Human CYP
11	20	100.0	13035	8	Aad41239 Human CYP
12	20	100.0	15185	8	Aad51997 Human CYP
13	20	100.0	39071	12	Aad52000 Human CYP
14	20	100.0	96960	8	Adm97420 Prostate
15	20	100.0	96960	8	Ac62734 Cancer ba
16	20	100.0	96960	10	AdB20849 MRPI base
17	20	100.0	96960	10	AdB87938 Human UGT
18	20	100.0	96960	10	AdB96921 Human MDR
19	20	100.0	123785	10	AdB92112 Human MDR
20	17.4	87.0	478	9	Abx77171 DNA sequ
					ACH33392 Human end

c	21	17.4	87.0	57502	12	ADQ97092	Adq97092 Human can
c	22	17	85.0	349980	5	AAH68527	Aah68527 C Glutami
c	23	16.8	84.0	3177	5	AAH13624	Aaah13624 CDNA sequ
c	24	16.8	84.0	90541	6	AB552847	Ab552847 Human SR
c	25	16.8	84.0	90541	10	ADJ37690	Adj37690 Human kin
c	26	16.8	84.0	90541	13	ADR31219	Adr31219 Human SRP
c	27	16.8	84.0	113033	8	AAH54213	Aaah54213 SR protei
c	28	16.8	84.0	219352	13	ABD33098	Abd33098 Murine ca
c	29	16.8	84.0	220224	11	ACN44702	Acn44702 Human gen
c	30	16.4	82.0	419	3	ADP58956	Adp58956 Urogenita
c	31	16.4	82.0	578	13	ACN46327	Acn46327 Cotton pr
c	32	16.4	82.0	870	5	AAH65731	Aah65731 C Glutami
c	33	16.4	82.0	990	4	AAH71019	Aah71019 C. glutam
c	34	16.4	82.0	1425	8	ACA53659	Acas3659 Prokaryot
c	35	16.4	82.0	114693	8	AAD48308	Adad48308 Human tra
c	36	16.4	82.0	118384	10	ABX56555	Abx56555 Human aut
c	37	16.4	82.0	349980	5	AAH68526	Aah68526 C glutami
c	38	15.8	79.0	65	6	ABN30407	Abn30407 Rat splic
c	39	15.8	79.0	233	6	ABL84451	Ab184451 Human ova
c	40	15.8	79.0	305	2	AAV87197	Aav87197 EST clone
c	41	15.8	79.0	308	4	ABA71670	Abat71670 Human foe
c	42	15.8	79.0	308	4	AAI51966	Aai51966 Probe #20
c	43	15.8	79.0	308	4	AAK46056	Aak46056 Human bon
c	44	15.8	79.0	308	4	AAK20014	Aak20014 Human bra
c	45	15.8	79.0	308	4	ABS45762	Abas45762 Human liv

#### ALIGNMENTS

#### RESULT 1

ABK68751

ID ABK68751 standard; DNA; 20 BP.

XX

AC ABK68751;

XX

DT 02-JUL-2002 (first entry)

XX

DE PCR primer #1 for detecting SNP in 5'-region of human CYP3A4 gene.

XX

KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;

XX PCR; primer; ss.

XX Homo sapiens.

XX

PN WO200218641-A2.

XX

PD 07-MAR-2002.

XX

PF 30-AUG-2001; 2001WO-IB001580.

XX

PR 30-AUG-2000; 2000GB-00021286.

XX

PA (GEMI-) GEMINI GENOMICS PLC.

XX

PI Risinger C, Andersson MK, Lewander T, Olaisson B;

XX

DR WPI; 2002-351712/38.

XX

PT Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5' flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes respectively.

XX

PS Claim 2; Page 15; 47pp; English.

XX

CC The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleotides for detecting single nucleotide polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450 (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position 461 of a defined 1345 base pair sequence for CYP3A4 or position 957, 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9. The PCR primers are useful for amplifying the CYP sequences and the

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 96.5227 Seconds  
(without alignments)  
4337.914 Million cell updates/sec

Title: US-09-943-115A-15

Perfect score: 11

Sequence: 1 gtgtgtacagc 11

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST:

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	67	CN869358	001202AAC
2	11	100.0	70	AI379030	tc53f01.x
3	11	100.0	70	AZ875009	AZ875009 2M0189A19
4	11	100.0	71	AZ936554	AZ936554 2M0193K13
5	11	100.0	85	CR181730	Reverse s
6	11	100.0	93	CR440674	CR440674 CR440674
7	11	100.0	100	CB395011	OSTR147F2
8	11	100.0	103	CV364386	PM1-GN030
9	11	100.0	104	BI017585	PM3-ET027
10	11	100.0	106	CR058606	Reverse s
11	11	100.0	108	BF334323	RC3-CT025
12	11	100.0	110	AJ709561	AJ709561 AJ709561
13	11	100.0	112	CG626392	OST334302
14	11	100.0	113	CV327048	CM4-UT004
15	11	100.0	113	BH367369	AG-ND-142
16	11	100.0	114	AA703431	z1j3a08.s
17	11	100.0	114	AZ537048	AST-2P014
18	11	100.0	115	BF988196	PM2-GN001
19	11	100.0	116	BF840511	RC6-HT100
20	11	100.0	119	BZ752975	PUPFA767D
21	11	100.0	121	BM481440	533678 MA
22	11	100.0	123	CD267768	tab10b04
23	11	100.0	123	CV349851	MR2-NT013
24	11	100.0	130	BG315020	OP3-0.115

C 25	11	100.0	130	9	CL693344
26	11	100.0	131	2	AW837764
C 27	11	100.0	133	1	AA426670
28	11	100.0	134	8	BZ642070
29	11	100.0	135	7	CN561395
30	11	100.0	135	8	CC178808
C 31	11	100.0	136	8	AZ664763
C 32	11	100.0	139	1	AA095286
33	11	100.0	139	2	BF739127
34	11	100.0	139	8	BZ274920
35	11	100.0	140	9	CG732105
C 36	11	100.0	142	2	BF935318
C 37	11	100.0	145	4	BI133732
C 38	11	100.0	148	5	BP094741
C 39	11	100.0	149	2	BF092197
40	11	100.0	150	8	CC065392
41	11	100.0	150	9	AG269438
42	11	100.0	151	1	AV041964
43	11	100.0	153	2	BF172673
44	11	100.0	154	8	B62266
C 45	11	100.0	155	7	CK192778

## ALIGNMENTS

RESULT 1  
CN869358  
LOCUS  
DEFINITION  
001202AAC006226HT (AAOA) Royal Gala phloem Malus x domestica CDNA  
clone AAOA006226, mRNA sequence.  
67 bp mRNA linear EST 03-JUN-2004  
CN869358  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Malus x domestica (cultivated apple)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
REFERENCE  
AUTHORS  
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,  
McAtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.  
TITLE  
JOURNAL  
COMMENT  
HortResearch Apple EST Project  
Unpublished (2004)  
Contact: Gleave, A.  
Sequencing Facility  
The Horticulture and Food Research Institute of New Zealand Ltd  
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand  
Tel: 00 64 09 815 4200  
Fax: 00 64 09 815 4201  
Email: est@hortresearch.co.nz.  
Location/Qualifiers  
1. 67  
/organism="Malus x domestica"  
/mol\_type="mRNA"  
/db\_xref="taxon:3750"  
/clone="AAOA006226"  
/tissue\_type="Phloem, scrapings from inside of bark mature wood"  
/clone\_lib="(AAOA) Royal Gala phloem"  
/note="Vector: pBluescript SK(-); Library sequenced by  
Genesis Research & Development"

## FEATURES

source

## ORIGIN

Query Match

Best Local Similarity 100.0%; Score 11; DB 7; Length 67;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GTGTGTACAGC 11

Db 43 GTGTGTACAGC 53

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 61.867 Seconds  
(without alignments)  
1103.355 Million cell updates/sec

Title: US-09-943-115A-15

Perfect score: 11

Sequencing: 1 gtgtgtacagc 11

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	10	US-09-943-115A-15
2	11	100.0	11	10	Sequence 15, Appl
3	11	100.0	25	21	US-09-943-115A-16
4	11	100.0	25	21	Sequence 16, Appl
5	11	100.0	25	21	Sequence 13901, A
6	11	100.0	25	21	Sequence 13901, A
7	11	100.0	25	21	Sequence 69725, A
					Sequence 136326, A
					Sequence 157636, A
					Sequence 273308, A

C 8	11	100.0	25	21	US-10-719-900-439658
C 9	11	100.0	25	21	US-10-719-900-539744
C 10	11	100.0	25	21	US-10-719-900-552782
C 11	11	100.0	25	21	US-10-719-900-573524
C 12	11	100.0	25	21	US-10-719-900-573525
C 13	11	100.0	25	21	US-10-719-900-573525
C 14	11	100.0	25	21	US-10-719-900-538285
C 15	11	100.0	25	21	US-10-719-900-709974
C 16	11	100.0	25	21	US-10-719-900-741261
C 17	11	100.0	25	21	US-10-719-900-765849
C 18	11	100.0	25	21	US-10-719-900-789331
C 19	11	100.0	25	21	US-10-719-900-838664
C 20	11	100.0	25	21	US-10-719-900-838665
C 21	11	100.0	25	21	US-10-719-900-976687
C 22	11	100.0	25	21	US-10-809-189-29335
C 23	11	100.0	25	21	US-10-809-189-29335
C 24	11	100.0	25	21	US-10-809-189-29335
C 25	11	100.0	25	21	US-10-809-189-29335
C 26	11	100.0	25	21	US-10-809-189-29335
C 27	11	100.0	25	21	US-10-809-189-29335
C 28	11	100.0	25	21	US-10-809-189-29335
C 29	11	100.0	25	21	US-10-809-189-29335
C 30	11	100.0	25	21	US-10-809-189-29335
C 31	11	100.0	25	21	US-10-809-189-29335
C 32	11	100.0	25	21	US-10-809-189-29335
C 33	11	100.0	25	21	US-10-809-189-29335
C 34	11	100.0	25	21	US-10-809-189-29335
C 35	11	100.0	25	21	US-10-809-189-29335
C 36	11	100.0	25	21	US-10-809-189-29335
C 37	11	100.0	25	21	US-10-809-189-29335
C 38	11	100.0	25	21	US-10-809-189-29335
C 39	11	100.0	25	21	US-10-809-189-29335
C 40	11	100.0	25	21	US-10-809-189-29335
C 41	11	100.0	25	21	US-10-809-189-29335
C 42	11	100.0	25	21	US-10-809-189-29335
C 43	11	100.0	25	21	US-10-809-189-29335
C 44	11	100.0	25	21	US-10-809-189-29335
C 45	11	100.0	25	21	US-10-809-189-29335

#### ALIGNMENTS

RESULT 1

US-09-943-115A-15

Sequence 15, Application US/09943115A

Publication No. US20030017469A1

GENERAL INFORMATION:

APPLICANT: SEQUENOM, Inc.

APPLICANT: Risinger, Carl

APPLICANT: Anderson, Maria

APPLICANT: Lewander, Tommy

APPLICANT: Olaisson, Erik

TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9

FILE REFERENCE: POLYMORPHISMS

FILE REFERENCE: 52459-20021.00

CURRENT APPLICATION NUMBER: US/09/943,115A

CURRENT FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: UK 0021286.0

PRIOR FILING DATE: 2000-08-30

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15

LENGTH: 11

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide of the novel polymorphic site 461

OTHER INFORMATION: on the coding strand

US-09-943-115A-15

Query Match 100.0%; Score 11; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:12:33 ; Search time 10.9221 Seconds  
(without alignments)  
5961.965 Million cell updates/sec

Title: US-09-943-115A-15

Perfect score: 11

Sequence: 1 gtgtgtacagc 11

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
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3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002as:\*  
7: Geneseq2002bs:\*  
8: Geneseq2003as:\*  
9: Geneseq2003bs:\*  
10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004as:\*  
13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	11	6	ABK68760 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 2	11	100.0	11	6	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 3	11	100.0	50	6	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 4	11	100.0	65	6	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 5	11	100.0	83	3	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 6	11	100.0	137	3	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 7	11	100.0	154	4	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 8	11	100.0	155	2	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 9	11	100.0	155	2	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 10	11	100.0	168	3	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 11	11	100.0	169	3	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 12	11	100.0	195	12	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 13	11	100.0	201	12	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 14	11	100.0	201	12	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 15	11	100.0	202	3	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 16	11	100.0	233	3	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 17	11	100.0	245	2	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 18	11	100.0	250	5	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 19	11	100.0	252	2	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
C 20	11	100.0	252	8	ABK68759 Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.

C 21	11	100.0	257	4	AAS24522 Human ova
C 22	11	100.0	259	8	ABZ19547 Group III
C 23	11	100.0	259	8	ABZ19547 Group III
C 24	11	100.0	259	8	ABZ19547 Group III
C 25	11	100.0	260	12	ACH83323 Human gen
C 26	11	100.0	261	12	ADJ25701 DNA encod
C 27	11	100.0	269	5	AAS81552 DNA encod
C 28	11	100.0	291	3	AAC24490 Human sec
C 29	11	100.0	292	6	ABN96731 Gene #322
C 30	11	100.0	305	5	AAS79399 DNA encod
C 31	11	100.0	305	13	ADRI13241 Human can
C 32	11	100.0	309	5	AAH81601 Human dif
C 33	11	100.0	331	9	ACH28094 Human adu
C 34	11	100.0	332	9	ACH24679 Human adu
C 35	11	100.0	334	3	AAC16060 Human sec
C 36	11	100.0	340	4	AAK78102 Human imm
C 37	11	100.0	340	4	AAK78102 Human imm
C 38	11	100.0	340	8	ADA41626 Human sec
C 39	11	100.0	340	8	ADA41627 Human sec
C 40	11	100.0	340	10	ADA57762 BAC fragm
C 41	11	100.0	340	10	ADA57763 BAC fragm
C 42	11	100.0	362	13	ADQ51775 Novel can
C 43	11	100.0	365	5	AAH83130 Human ova
C 44	11	100.0	367	2	AAV86729 EST clone
C 45	11	100.0	377	11	ADP65928 Mouse EST

## ALIGNMENTS

RESULT 1  
ABK68760/c  
ID ABK68760 standard; DNA; 11 BP.

AC ABK68760;

DT 02-JUL-2002 (first entry)

DE Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.

XX Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4; ss.

OS Homo sapiens.

XX WO200218641-A2.

PD 07-MAR-2002.

PF 30-AUG-2001; 2001WO-18001580.

PR 30-AUG-2000; 2000GB-00021286.

XX (GEMINI-) GEMINI GENOMICS PLC.

PA Risinger C, Andersson MK, Lewander T, Olafsson E; WPI; 2002-351712/38.

XX Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5' flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes respectively.

PS Claim 4; Page 17; 47pp; English.

XX The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleotides for detecting single nucleotide polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450 (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position 461 of a defined 1345 base pair sequence for CYP3A4 or position 957, 1049, 1164, 1536, 1661 and 1662 of a 2438 base pair sequence for CYP2C9. The PCR primers are useful for amplifying the CYP sequences and the

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 19:46:29 ; Search time 3.1551 Seconds  
(without alignments)  
5704.747 Million cell updates/sec

Title: US-09-943-115A-15  
Perfect score: 11  
Sequence: 1 GTGTGTACAGC 11

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	25	4	US-09-396-196G-29335
C 2	11	100.0	25	4	US-09-396-196G-69385
C 3	11	100.0	83	4	US-09-513-999C-12960
4	11	100.0	146	1	US-08-062-472B-33
C 5	11	100.0	168	4	US-09-513-999C-34370
C 6	11	100.0	202	4	US-09-513-999C-35483
C 7	11	100.0	221	4	US-09-270-767-6886
C 8	11	100.0	221	4	US-09-270-767-22168
C 9	11	100.0	233	4	US-09-513-999C-10146
10	11	100.0	291	4	US-09-513-999C-28565
11	11	100.0	334	4	US-09-513-999C-20135
12	11	100.0	370	4	US-09-621-976-9081
C 13	11	100.0	430	4	US-09-513-999C-413
14	11	100.0	438	4	US-09-949-016-916
15	11	100.0	438	4	US-09-949-016-4050
16	11	100.0	447	3	US-08-903-139B-17
C 17	11	100.0	447	4	US-09-270-767-5014
C 18	11	100.0	447	4	US-09-270-767-20296
C 19	11	100.0	480	4	US-09-710-275-763
C 20	11	100.0	482	4	US-09-513-999C-3947
21	11	100.0	490	3	US-09-348-884-3
22	11	100.0	517	4	US-09-270-767-3142
23	11	100.0	517	4	US-09-270-767-18424
C 24	11	100.0	517	4	US-09-854-133-671
25	11	100.0	518	4	US-09-621-976-3448
C 26	11	100.0	595	3	US-09-740-235-6
C 27	11	100.0	601	4	US-09-949-016-18083

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28 11 100.0 601 4 US-09-949-016-22957
29 11 100.0 601 4 US-09-949-016-24858
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36 11 100.0 601 4 US-09-949-016-30005
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42 11 100.0 601 4 US-09-949-016-65812
C 43 11 100.0 601 4 US-09-949-016-71259
C 44 11 100.0 601 4 US-09-949-016-71260
C 45 11 100.0 601 4 US-09-949-016-71261

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## ALIGNMENTS

RESULT 1  
US-09-396-196G-29335  
; Sequence 29335, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Lockhart  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29335  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-29335

Query Match: 100.0%; Score 11; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTGTGTACAGC 11  
Db 9 GTGTGTACAGC 19

RESULT 2  
US-09-396-196G-69385/c  
; Sequence 69385, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Lockhart  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69385

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 96.5227 Seconds  
(without alignments)  
4337.914 Million cell updates/sec

Title: US-09-943-115A-16

Perfect score: 11

Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:

1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_est4:  
5: gb\_est5:  
6: gb\_est6:  
7: gb\_est7:  
8: gb\_est8:  
9: gb\_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 3	11	100.0	70	8	A2875009
C 4	11	100.0	71	8	A2936554
C 5	11	100.0	85	9	CR181730
C 6	11	100.0	93	7	CR440674
C 7	11	100.0	100	6	CB395011
C 8	11	100.0	103	7	CV364386
C 9	11	100.0	104	4	B1017585
C 10	11	100.0	106	9	CR058606
C 11	11	100.0	108	2	BF334323
C 12	11	100.0	110	1	AJ709561
C 13	11	100.0	112	9	CG626392
C 14	11	100.0	113	7	CV327048
C 15	11	100.0	113	8	BH367369
C 16	11	100.0	114	1	AA703431
C 17	11	100.0	114	8	A2537048
C 18	11	100.0	115	4	BF988196
C 19	11	100.0	116	2	BF840511
C 20	11	100.0	119	8	BZ752975
C 21	11	100.0	121	4	BM481440
C 22	11	100.0	123	6	CD267768
C 23	11	100.0	123	7	CV349851
C 24	11	100.0	130	4	BG315020

25 11 100.0 130 9 CL693344  
c 26 11 100.0 131 2 AW837764  
27 11 100.0 133 1 AA426670  
c 28 11 100.0 134 8 BZ642070  
c 29 11 100.0 135 7 CN561395  
c 30 11 100.0 135 8 CCL78808  
31 11 100.0 136 8 A2664763  
c 32 11 100.0 139 1 AA095286  
c 33 11 100.0 139 2 BF739127  
c 34 11 100.0 139 8 BZ274920  
c 35 11 100.0 140 9 CG732105  
36 11 100.0 142 2 BF935318  
37 11 100.0 145 4 B1133732  
38 11 100.0 148 5 BP094741  
39 11 100.0 149 2 BF092197  
c 40 11 100.0 150 8 CC065392  
c 41 11 100.0 150 9 AG269438  
c 42 11 100.0 151 1 AV041964  
c 43 11 100.0 153 2 BF172673  
c 44 11 100.0 154 8 B62266  
c 45 11 100.0 155 7 CK192778

#### ALIGNMENTS

RESULT 1  
CN869358/4  
LOCUS  
DEFINITION 001202AAOA006226HT (AAOA) Royal Gala phloem Malus x domestica cDNA  
clone AAOA006226, mRNA sequence.  
ACCESSION  
CN869358  
VERSION  
CN869358.1 GI:48126987  
KEYWORDS  
EST.  
SOURCE  
Malus x domestica (cultivated apple)  
ORGANISM  
Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
REFERENCE  
1 (bases 1 to 57)  
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y. HortResearch Apple EST-Project Unpublished (2004)  
JOURNAL  
COMMENT  
Contact: Gleave, A.  
Sequencing Facility  
The Horticulture and Food Research Institute of New Zealand Ltd  
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand  
Tel: 00 64 09 815 4200  
Fax: 00 64 09 815 4201  
Email: est@hortresearch.co.nz.  
FEATURES  
source  
1. 67  
/organism="Malus x domestica"  
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/db\_xref="taxon:3750"  
/clone="AAOA006226"  
/tissue\_type="Phloem, scrapings from inside of bark mature wood"  
/clone\_lib=" (AAOA) Royal Gala phloem"  
/notes="Vector: pBluescript SK(-); Library sequenced by Genesis Research & Development"

Query Match 100.0%; Score 11; DB 7; Length 67;  
Best Local Similarity 100.0%; Pred. No. 4.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTGTACACAC 11  
Dd 53 GCTGTACACAC 43

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 61.8867 Seconds  
(without alignments)  
1103.355 Million cell updates/sec

Title: US-09-943-115A-16  
Perfect score: 11  
Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues  
Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
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- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
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- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 3	11	100.0	25	21	US-10-719-900-13901
C 4	11	100.0	25	21	US-10-719-900-69725
C 5	11	100.0	25	21	US-10-719-900-136326
C 6	11	100.0	25	21	US-10-719-900-157636
C 7	11	100.0	25	21	US-10-719-900-273308

Sequence 439658,	25	21	US-10-719-900-439658
Sequence 539744,	25	21	US-10-719-900-539744
Sequence 55782,	25	21	US-10-719-900-55782
Sequence 573524,	25	21	US-10-719-900-573524
Sequence 573525,	25	21	US-10-719-900-573525
Sequence 638285,	25	21	US-10-719-900-638285
Sequence 709974,	25	21	US-10-719-900-709974
Sequence 741261,	25	21	US-10-719-900-741261
Sequence 765849,	25	21	US-10-719-900-765849
Sequence 789331,	25	21	US-10-719-900-789331
Sequence 838664,	25	21	US-10-719-900-838664
Sequence 838665,	25	21	US-10-719-900-838665
Sequence 976687,	25	21	US-10-719-900-976687
Sequence 29335, A	25	21	US-10-809-189-29335
Sequence 69385, A	25	21	US-10-809-189-69385
Sequence 233704,	25	21	US-10-956-157-233704
Sequence 435, App	50	17	US-10-131-827-435
Sequence 4847, Ap	65	10	US-09-908-975-4847
Sequence 3917, Ap	103	9	US-09-783-590-3917
Sequence 5639, Ap	109	19	US-10-674-124A-5639
Sequence 1783, Ap	110	19	US-10-674-124A-1783
Sequence 32776, A	154	9	US-09-864-761-32776
Sequence 19639, A	162	19	US-10-674-124A-19639
Sequence 19294, A	172	19	US-10-674-124A-19294
Sequence 2012, Ap	187	18	US-10-424-599-2012
Sequence 21601, A	194	19	US-10-674-124A-21601
Sequence 15563, A	195	16	US-10-029-386-15563
Sequence 11490, A	201	19	US-10-741-601-11490
Sequence 11492, A	201	19	US-10-741-601-11492
Sequence 12160, A	201	19	US-10-741-601-12160
Sequence 24597, A	201	19	US-10-741-601-24597
Sequence 29823, A	201	21	US-10-741-600-29823
Sequence 66110, A	201	21	US-10-741-600-66110
Sequence 9514, Ap	202	19	US-10-674-124A-9514
Sequence 14106, A	216	19	US-10-674-124A-14106
Sequence 86457, A	228	18	US-10-424-599-86457
Sequence 1144, Ap	235	19	US-10-674-124A-1144
Sequence 58061, A	241	18	US-10-424-599-58061

ALIGNMENTS

RESULT 1  
US-09-943-115A-15/c  
; Sequence 15, Application US/09943115A  
; Publication No. US20030017469A1  
; GENERAL INFORMATION:  
; APPLICANT: SEQUENOM, Inc.  
; APPLICANT: Risinger, Carl  
; APPLICANT: Andersson, Maria  
; APPLICANT: Lewander, Tommy  
; APPLICANT: Olsson, Erik  
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9  
; TITLE OF INVENTION: POLYMORPHISMS  
; FILE REFERENCE: 52459-20021.00  
; CURRENT APPLICATION NUMBER: US/09/943.115A  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: UK 0021286.0  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide of the novel polymorphic site 461  
; OTHER INFORMATION: on the coding strand  
US-09-943-115A-15

Query Match 100.0% Score 11; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 19:46:29 ; Search time 3.1551 Seconds  
(without alignments)  
5704.747 Million cell updates/sec

Title: US-09-943-115A-16

Perfect score: 11

Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:

- 1: /cgn2\_6/prodata/1/ina/5A-COMB.seq:\*\*
- 2: /cgn2\_6/prodata/1/ina/5B-COMB.seq:\*\*
- 3: /cgn2\_6/prodata/1/ina/6A-COMB.seq:\*\*
- 4: /cgn2\_6/prodata/1/ina/6B-COMB.seq:\*\*
- 5: /cgn2\_6/prodata/1/ina/PCYUS-COMB.seq:\*\*
- 6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	25	4	US-09-396-196G-29335, A
C 2	11	100.0	25	4	US-09-396-196G-29335, A
C 3	11	100.0	83	4	US-09-513-999C-12960, A
C 4	11	100.0	146	1	US-08-062-4728-33, Appl
C 5	11	100.0	168	4	US-09-513-999C-34370, A
C 6	11	100.0	202	4	US-09-513-999C-35483, A
C 7	11	100.0	221	4	US-09-270-767-6886, Ap
C 8	11	100.0	221	4	US-09-270-767-22168, A
C 9	11	100.0	233	4	US-09-513-999C-10146, A
C 10	11	100.0	291	4	US-09-513-999C-28565, A
C 11	11	100.0	334	4	US-09-513-999C-20135, A
C 12	11	100.0	370	4	US-09-621-976-9081, Ap
C 13	11	100.0	430	4	US-09-513-999C-413, App
C 14	11	100.0	438	4	US-09-949-016-916, App
C 15	11	100.0	438	4	US-09-949-016-4050, App
C 16	11	100.0	443	3	US-08-903-1398-17, Appl
C 17	11	100.0	447	4	US-09-270-767-5014, Ap
C 18	11	100.0	447	4	US-09-270-767-20296, A
C 19	11	100.0	480	4	US-09-710-279-763, App
C 20	11	100.0	482	4	US-09-513-999C-3947, Ap
C 21	11	100.0	490	3	US-09-349-884-3, Appl
C 22	11	100.0	517	4	US-09-270-767-3142, Ap
C 23	11	100.0	517	4	US-09-270-767-18424, A
C 24	11	100.0	517	4	US-09-854-133-671, App
C 25	11	100.0	518	4	US-09-621-976-3448, App
C 26	11	100.0	595	3	US-09-740-235-6, Appl
C 27	11	100.0	601	4	US-09-949-016-18083, A

#### ALIGNMENTS

##### RESULT 1

US-09-396-196G-29335/c  
; Sequence 29335, Application US/09396196G  
; Patent No. 6821724

##### GENERAL INFORMATION:

; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29335  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-29335

Query Match 100.0%; Score 11; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGTACACAC 11  
|||||  
Db 19 GCTGTACACAC 9

##### RESULT 2

US-09-396-196G-69385  
; Sequence 69385, Application US/09396196G  
; Patent No. 6821724

##### GENERAL INFORMATION:

; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69385

C 28 11 100.0 601 4 US-09-949-016-22957, A  
C 29 11 100.0 601 4 US-09-949-016-24858, A  
C 30 11 100.0 601 4 US-09-949-016-24859, A  
C 31 11 100.0 601 4 US-09-949-016-25315, A  
C 32 11 100.0 601 4 US-09-949-016-25316, A  
C 33 11 100.0 601 4 US-09-949-016-26336, A  
C 34 11 100.0 601 4 US-09-949-016-26337, A  
C 35 11 100.0 601 4 US-09-949-016-29322, A  
C 36 11 100.0 601 4 US-09-949-016-30005, A  
C 37 11 100.0 601 4 US-09-949-016-35609, A  
C 38 11 100.0 601 4 US-09-949-016-35610, A  
C 39 11 100.0 601 4 US-09-949-016-35611, A  
C 40 11 100.0 601 4 US-09-949-016-36230, A  
C 41 11 100.0 601 4 US-09-949-016-63015, A  
C 42 11 100.0 601 4 US-09-949-016-65812, A  
C 43 11 100.0 601 4 US-09-949-016-71259, A  
C 44 11 100.0 601 4 US-09-949-016-71260, A  
C 45 11 100.0 601 4 US-09-949-016-71261, A



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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:12:33 ; Search time 10.9221 Seconds  
(without alignments)  
5961.965 Million cell updates/sec

Title: US-09-943-115A-16  
Perfect score: 11  
Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	6	ABK68760
2	11	100.0	11	6	ABK68759
3	11	100.0	50	6	ABZ00444
4	11	100.0	65	6	ABN32099
5	11	100.0	83	3	AA008885
6	11	100.0	137	3	AA43131
7	11	100.0	154	4	AA149406
8	11	100.0	155	2	AAH85562
9	11	100.0	155	2	AAH85561
10	11	100.0	168	3	AA030295
11	11	100.0	169	3	AA48201
12	11	100.0	195	12	ACH82368
13	11	100.0	201	12	ADM97390
14	11	100.0	201	12	ADM97385
15	11	100.0	202	3	AA031408
16	11	100.0	233	3	AA06071
17	11	100.0	245	2	AAQ76753
18	11	100.0	250	5	ABV48999
19	11	100.0	252	2	AAQ60885
20	11	100.0	252	8	ABX39550

21	11	100.0	257	4	AA524522
22	11	100.0	259	8	ABZ19547
23	11	100.0	259	8	ABZ19167
24	11	100.0	259	8	ABZ19345
25	11	100.0	260	12	ACH83323
26	11	100.0	261	12	ADJ25701
27	11	100.0	269	5	AA581552
28	11	100.0	291	3	AA024490
29	11	100.0	292	6	ABN96731
30	11	100.0	302	5	AA579399
31	11	100.0	305	13	ADRI3241
32	11	100.0	309	5	AAH81601
33	11	100.0	331	9	ACH28094
34	11	100.0	332	3	ACH24679
35	11	100.0	334	3	AA016060
36	11	100.0	340	4	AAK78102
37	11	100.0	340	4	AAK78104
38	11	100.0	340	8	ADA41626
39	11	100.0	340	8	ADA41627
40	11	100.0	340	10	ADA57762
41	11	100.0	340	10	ADA57763
42	11	100.0	362	13	ADQ51775
43	11	100.0	365	5	AAH83130
44	11	100.0	367	2	AAV86729
45	11	100.0	377	11	ADP65928

## ALIGNMENTS

## RESULT 1

ABK68760  
ID ABK68760 standard; DNA; 11 BP.

XX AC ABK68760;

XX 02-JUL-2002 (first entry)

DE Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.

XX Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4; ss.

XX Homo sapiens.

XX WO200218641-A2.

XX 07-MAR-2002.

XX 30-AUG-2001; 2001WO-IB001580.

XX 30-AUG-2000; 2000GB-00021286.

XX (GEMI-) GEMINI GENOMICS PLC.

XX Risinger C, Andersson MK, Lewander T, Olafsson E;

XX WPI; 2002-351712/38.

XX Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5' flanking regions of cytochrome p450 (CYP) 3A4 and CYP2C9 genes respectively.

XX Claim 4; Page 17; 47pp; English.

XX The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleotides for detecting single nucleotide polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450 (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position 461 of a defined 1345 base pair sequence for CYP3A4 or position 957, 1049, 1164, 1526, 1661 and 1862 of a 2438 base pair sequence for CYP2C9. The PCR primers are useful for amplifying the CYP sequences and the

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:18:28 ; Search time 56.1997 Seconds  
(without alignments)  
9484.165 Million cell updates/sec

Title: US-09-943-115A-15

Perfect score: 11

Sequence: 1 gtgtgtacagc 11

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb\_in.\*

4: gb\_om.\*

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6: gb\_pa.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	6	AX421267 Sequence
2	11	100.0	11	6	AX421268 Sequence
3	11	100.0	60	6	A29455 Sequence ex
4	11	100.0	61	9	HUMTCDV1DG
5	11	100.0	65	6	CQ535212 Sequence
6	11	100.0	83	6	AX897097 Sequence
7	11	100.0	83	6	BD032630 Sequence
8	11	100.0	110	11	AU048812 Rattus no
9	11	100.0	123	11	AF235274
10	11	100.0	133	4	AY434952
11	11	100.0	146	6	I84526 Sequence 33
12	11	100.0	153	11	GI8652
13	11	100.0	154	6	CQ109233 Sequence
14	11	100.0	163	11	BV101004
15	11	100.0	168	6	AX918507 Sequence
16	11	100.0	168	6	BD054040 Sequence
17	11	100.0	169	9	HSU52166
18	11	100.0	188	5	AB010782 Hexagramm
19	11	100.0	194	11	AF253624 Sus scrofa

20	11	100.0	201	11	BV205410
21	11	100.0	202	6	AX919620 Sequence
22	11	100.0	202	6	BD055153 Sequence
23	11	100.0	204	6	CQ748128 Sequence
24	11	100.0	221	6	ARS01926 Sequence
25	11	100.0	221	6	ARS17208 Sequence
26	11	100.0	221	6	AX894283 Sequence
27	11	100.0	233	6	BD029816 Sequence
28	11	100.0	233	5	AF330225
29	11	100.0	235	5	CR390323
30	11	100.0	244	5	SSA402851
31	11	100.0	245	6	A74667
32	11	100.0	245	6	A77646
33	11	100.0	248	9	HS265VB1
34	11	100.0	248	11	AF013210
35	11	100.0	250	6	CQ517151
36	11	100.0	256	11	AU026314
37	11	100.0	257	6	AX208863
38	11	100.0	261	6	CQ765925
39	11	100.0	265	11	G25356
40	11	100.0	273	11	AU028591
41	11	100.0	273	5	HCH388044
42	11	100.0	281	6	CQ703253
43	11	100.0	287	11	G64262
44	11	100.0	291	6	AX912702
45	11	100.0	291	6	BD048235

## ALIGNMENTS

RESULT 1	AX421267	11 bp	DNA	linear	PAT 18-JUN-2002
LOCUS	Sequence 15 from Patent WO0218641.				
DEFINITION	AX421267				
ACCESSION	AX421267.1				
VERSION	AX421267.1	GI:21524675			
KEYWORDS	synthetic construct				
SOURCE	other sequences; artificial sequences.				
ORGANISM	Risinger, C., Andersson, M.K., Lewander, T. and Olaisson, E.				
REFERENCE	Detection of cyp3a4 and cyp2c9 polymorphisms				
AUTHORS	Patent: WO 0218641-A 15 07-MAR-2002;				
TITLE	Gemini Genomics PLC (GB)				
JOURNAL	Location/Qualifiers				
FEATURES	1..11				
source	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Oligonucleotide of the novel polymorphic site 461 on the coding strand"				

## ORIGIN

Query Match	100.0%;	Score 11;	DB 6;	Length 11;	
Best Local Similarity	100.0%;	Pred. No. 7.3e+04;			
Matches	11;	Conservative	0;	Mismatches 0;	
				Indels 0; Gaps 0;	
Qy	1	GTGTGTACAGC 11			
Db	1	GTGTGTACAGC 11			
RESULT 2	AX421268/c	11 bp	DNA	linear	PAT 18-JUN-2002
LOCUS	Sequence 16 from Patent WO0218641.				
DEFINITION	AX421268				
ACCESSION	AX421268				
VERSION	AX421268.1	GI:21524676			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:18:28 ; Search time 56.1997 Seconds  
(without alignments)  
9484.165 Million cell updates/sec

Title: US-09-943-115A-16  
Perfect score: 11  
Sequence: 1 gctgtacacac 11

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_scs.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	11	100.0	11	6	AX421267	AX421267 Sequence
C 2	11	100.0	11	6	AX421268	AX421268 Sequence
C 3	11	100.0	60	6	A29455	A29455 sequence ex
C 4	11	100.0	61	9	HUMICVDLDB	L32456 Human (clon
C 5	11	100.0	65	6	CQ535212	CQ535212 Sequence
C 6	11	100.0	83	6	AX897097	AX897097 Sequence
C 7	11	100.0	83	6	BD032630	BD032630 Sequence
C 8	11	100.0	110	11	AU048812	AU048812 Rattus no
C 9	11	100.0	123	11	AF235274	AF235274 Sus scrof
C 10	11	100.0	133	4	AX434952	AX434952 Felis cat
C 11	11	100.0	146	6	I84526	I84526 Sequence 33
C 12	11	100.0	153	11	G18652	G18652 BMS1304 cow
C 13	11	100.0	154	6	CQ109233	CQ109233 Sequence
C 14	11	100.0	163	11	BV101004	BV101004 RFAMWSEQ
C 15	11	100.0	168	6	AX918507	AX918507 Sequence
C 16	11	100.0	168	6	BD054040	BD054040 Sequence
C 17	11	100.0	169	9	H5U52166	U52166 Human tumor
C 18	11	100.0	188	5	AB010782	AB010782 Hexagramm
C 19	11	100.0	194	11	AF253624	AF253624 Sus scrof

C 20	11	100.0	201	11	BV205410	BV205410 sqmm21813
C 21	11	100.0	202	6	AX919620	AX919620 Sequence
C 22	11	100.0	202	6	BD055153	BD055153 Sequence
C 23	11	100.0	204	6	CQ748128	CQ748128 Sequence
C 24	11	100.0	221	6	AR501926	AR501926 Sequence
C 25	11	100.0	221	6	AR517208	AR517208 Sequence
C 26	11	100.0	233	6	AX894283	AX894283 Sequence
C 27	11	100.0	233	6	BD029816	BD029816 Sequence
C 28	11	100.0	235	5	AF330225	AF330225 Oncorhync
C 29	11	100.0	238	5	CR390323	CR390323 Gallus ga
C 30	11	100.0	244	5	SSA402851	AJ402851 Salmo sal
C 31	11	100.0	245	6	A74667	A74667 Sequence 35
C 32	11	100.0	245	6	A77646	A77646 Sequence 35
C 33	11	100.0	248	9	HS265VB1	Z23877 H. sapiens
C 34	11	100.0	248	11	AF013210	AQ013210 Rattus no
C 35	11	100.0	250	6	CQ517151	CQ517151 Sequence
C 36	11	100.0	256	11	AU026314	AU026314 Rattus no
C 37	11	100.0	257	6	AX208863	AX208863 Sequence
C 38	11	100.0	261	6	CQ765925	CQ765925 Sequence
C 39	11	100.0	265	11	G25356	G25356 human STS E
C 40	11	100.0	273	11	AU028591	AU028591 Rattus no
C 41	11	100.0	279	5	HCH388044	AJ388044 Hyla chry
C 42	11	100.0	281	6	CQ703253	CQ703253 Sequence
C 43	11	100.0	287	11	G64262	G64262 AMHR2/ex11
C 44	11	100.0	291	6	AX912702	AX912702 Sequence
C 45	11	100.0	291	6	BD048235	BD048235 Sequence

#### ALIGNMENTS

RESULT 1  
AX421267/c  
LOCUS AX421267 11 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 15 from Patent WO0218641.  
ACCESSION AX421267  
VERSION AX421267.1 GI:21524675  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Risinger,C., Anderson,M.K., Lewander,T. and Olaiasson,E.  
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms  
JOURNAL Patent: WO 0218641-A 15 07-MAR-2002;  
GEMINI Genomics PLC (GB)  
FEATURES  
source  
1..11  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/notes="Oligonucleotide of the novel polymorphic site 461 on the coding strand"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 11;  
Best local Similarity 100.0%; Pred. No. 7.3e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTGTACACAC 11  
DB 11 GCTGTACACAC 1  
RESULT 2  
AX421268  
LOCUS AX421268 11 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 16 from Patent WO0218641.  
ACCESSION AX421268  
VERSION AX421268.1 GI:21524676  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 18:55:11 ; Search time 11802.1 Seconds  
(without alignments)  
4337.914 Million cell updates/sec

Title: US-09-943-115A-1  
Perfect score: 1345  
Sequence: 1 ctgcagtgaccactgcccac.....cgtaacaggcctctctttt 1345

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_his:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsl:  
9: gb\_gsl2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413	30.7	606	AZ537700	HSC 00196
2	214.4	15.9	320	T60367	YB90H09.r1
3	200.8	14.9	633	AV646048	AV646048
4	186.6	13.9	872	CR810224	GR0AA33C
5	166.6	12.4	583	BP270511	BP270511
6	164.6	12.2	300	AU100464	AU100464
7	164.6	12.2	601	EX506284	DKF2p686I
8	164	12.2	582	BP270391	BP270391
9	163.6	12.2	599	BP383396	BP383396
10	162.4	12.1	650	AV654562	AV654562
11	160.6	11.9	358	AV660310	AV660310
12	156.4	11.6	364	AV655529	AV655529
13	153.6	11.4	584	AV657970	AV657970
14	152	11.3	298	CR788987	CR788987
15	151	11.2	755	EX643367	EX643367
16	150.8	11.2	771	AV646975	AV646975
17	147.8	11.0	411	TV1511	TV1511
18	144.6	10.8	262	T74622	YC57a05.r1
19	143.2	10.6	957	CO581316	CO581316
20	143	10.6	934	CO581493	CO581493
21	142.2	10.6	821	CO582079	CO582079
22	141	10.5	165	AU076847	AU076847
23	140	10.4	875	EX445330	EX445330
24	140	10.4	1090	EX428031	EX428031

25	139.8	10.4	870	7	CO583597	CO583597
26	139.8	10.4	943	7	CO583293	CO583293
27	138.8	10.4	982	7	CO581624	CO581624
28	138.6	10.4	947	5	EX388061	EX388061
29	139.2	10.3	938	5	EX422263	EX422263
30	139	10.3	314	7	T68354	YC41c05.r1
31	137.4	10.2	380	5	EX494898	DKF2p779E
32	137.4	10.2	2192	6	CD013971	CD013971
33	137	10.2	922	5	EX463042	EX463042
34	137	10.2	942	1	AL531737	AL531737
35	136	10.1	734	7	CF271965	CF271965
36	136	10.1	748	7	CF271966	CF271966
37	136	10.1	778	7	CK130234	CK130234
38	136	10.1	779	7	CF271964	CF271964
39	136	10.1	780	7	CK130233	CK130233
40	135.8	10.1	841	5	EX449069	EX449069
41	135.2	10.1	681	5	EX951468	EX951468
42	134.4	10.0	749	7	CK130235	CK130235
43	133.8	9.9	550	6	CB122271	CB122271
44	132.4	9.8	676	5	EX476664	EX476664
45	132	9.8	571	4	EM837821	EM837821

## ALIGNMENTS

RESULT 1  
AZ537700  
LOCUS HSC 00196 RPCI-11 Human Male BAC Library Homo sapiens genomic clone  
DEFINITION H N0513J13, genomic survey sequence.  
ACCESSION AZ537700  
VERSION AZ537700.1 GI:11125732  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 606)  
AUTHORS Scherer, S.W., Rommens, J.M. and Tsui, L.C.  
TITLE Gene Identification on Human Chromosome 7  
JOURNAL Unpublished (2000)  
COMMENT Contact: Scherer, S.W.; Rommens, J.M.; Tsui, L.C.; Boright, A.P.  
The Human Chromosome 7 Project  
Department of Genetics, The Hospital for Sick Children  
555 University Avenue, Toronto, Ontario M5G 1X8, Canada  
Tel: 416 813 7613  
Fax: 416 813 8319  
Email: steve@genet.sickkids.on.ca  
Clone maps to 7q22 (contains CYP3A5, CYP3A7, D7S2432, D7S647, D7S1678, D7S2832)  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 606.  
Location/Qualifiers  
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/notes="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

FEATURES  
source  
1. 606  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/clone="H N0513J13"  
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/clone\_lib="RPCI-11 Human Male BAC Library"  
/notes="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

## ORIGIN

Query Match 30.7%; Score 413; DB 8; Length 606;  
Best Local Similarity 89.2%; Pred. No. 2.3e-108;  
Matches 502; Conservative 1; Mismatches 45; Indels 15; Gaps 5;

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 22:36:54 ; Search time 7567.05 Seconds  
(without alignments)  
1103.355 Million cell updates/sec

Title: US-09-943-115A-1

Perfect score: 1345

Sequence: 1 ctcagtcagccactgcccc.....cgtatcagcctctctttt 1345

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
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- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1344.2	99.9	1345	10	US-09-943-115A-1
2	1344.2	99.9	1345	14	US-10-146-575-3
3	1344.2	99.9	1345	14	US-10-085-612-3
4	1310	97.4	96960	21	US-10-484-577-662
5	1190.2	88.5	13035	15	US-10-121-960C-14
6	1153.2	85.7	15185	15	US-10-121-960C-17
7	1140.2	84.8	12983	21	US-10-415-607-1

8	924.4	68.7	11186	9	US-09-957-997-1	Sequence 1, Appli
9	924.4	68.7	11186	21	US-10-415-607-4	Sequence 4, Appli
10	813.2	60.5	1012	9	US-09-957-997-4	Sequence 4, Appli
11	646.4	48.1	8943	17	US-10-257-166-47	Sequence 47, Appl
12	578.8	43.0	8943	17	US-10-257-166-48	Sequence 48, Appl
13	518.4	38.5	177531	21	US-10-484-577-660	Sequence 660, App
14	496.8	36.9	1254	14	US-10-085-612-4	Sequence 149, App
15	309.6	23.0	8776	17	US-10-257-166-149	Sequence 150, App
16	237.4	17.7	8776	17	US-10-257-166-150	Sequence 151, App
17	227.4	16.9	96960	21	US-10-484-577-662	Sequence 662, App
18	177.6	13.2	2768	16	US-10-268-822-14	Sequence 14, Appl
19	177.6	13.2	2768	17	US-10-388-360-297	Sequence 297, App
20	177.6	13.2	2768	17	US-10-388-360-363	Sequence 363, App
21	163.6	12.2	2059	18	US-10-641-643-1062	Sequence 1062, Ap
22	136	10.1	1595	15	US-10-106-698-1724	Sequence 1724, Ap
23	135.6	10.1	2759	14	US-10-146-575-1	Sequence 1, Appli
24	135.2	10.1	2849	9	US-09-880-107-2110	Sequence 2110, Ap
25	123	9.1	2011	9	US-09-880-107-1586	Sequence 1586, Ap
26	119	8.8	1707	9	US-09-880-107-2114	Sequence 2114, Ap
27	119	8.8	1707	18	US-10-641-643-1060	Sequence 1060, Ap
28	118	8.8	384	9	US-09-925-297-24	Sequence 24, Appl
29	115.8	8.6	1659	13	US-10-007-814-1	Sequence 1, Appli
30	113.4	8.4	1915	18	US-10-112-944-188	Sequence 188, App
31	112	8.3	489	13	US-10-027-632-277590	Sequence 277590,
32	112	8.3	489	17	US-10-027-632-277590	Sequence 3816, Ap
33	107.4	8.0	1525	9	US-09-880-107-3816	Sequence 1405, Ap
34	107.4	8.0	1599	18	US-10-641-643-1405	Sequence 39, Appl
35	106	7.9	106	13	US-10-007-814-39	Sequence 40, Appl
36	88.4	6.6	106	13	US-10-007-814-40	Sequence 15077, A
37	74.6	5.5	105	13	US-10-007-814-41	Sequence 4176, Ap
38	74.6	5.5	240	9	US-09-960-352-15077	Sequence 6070, Ap
39	74.6	5.5	380	9	US-09-960-352-15107	Sequence 8232, Ap
40	74.6	5.5	411	9	US-09-960-352-4176	Sequence 55, Appl
41	74.6	5.5	422	9	US-09-960-352-6070	Sequence 3467, Ap
42	74.6	5.5	430	9	US-09-960-352-8232	
43	73.6	5.5	1512	17	US-10-313-963A-55	
44	73.2	5.4	207	9	US-09-960-352-9871	
45	73.2	5.4	347	9	US-09-960-352-3467	

ALIGNMENTS

RESULT 1  
US-09-943-115A-1  
; Sequence 1, Application US/09943115A  
; Publication No. US20030017469A1  
; GENERAL INFORMATION:  
; APPLICANT: SEQUENOM, Inc.  
; APPLICANT: Risinger, Carl  
; APPLICANT: Andersson, Maria  
; APPLICANT: Lewander, Tommy  
; APPLICANT: Olsson, Erik  
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9  
; TITLE OF INVENTION: POLYMORPHISMS  
; FILE REFERENCE: 52459-20021.00  
; CURRENT APPLICATION NUMBER: US/09/943.115A  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: UK 0021286.0  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1345  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-943-115A-1

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTGAGTGACCACTGCGCCCATCTTGTGCTGAGGTGGTGGTCCATCTGGCTATCT 60

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		Match	Length			
1	1344.2	99.9	1345	3	US-09-372-339-1	Sequence 1, Appli
2	1344.2	99.9	1345	3	US-09-372-339-2	Sequence 2, Appli
3	1344.2	99.9	1345	3	US-09-144-367-3	Sequence 3, Appli
4	1310	97.4	31197	4	US-09-949-016-12963	Sequence 12963, A
5	1310	97.4	103934	4	US-09-949-016-14433	Sequence 14433, A
6	1079.6	80.3	34172	4	US-09-949-016-14432	Sequence 14432, A
7	518.4	38.5	35803	4	US-09-949-016-11863	Sequence 11863, A
8	518.4	38.5	35804	4	US-09-949-016-12862	Sequence 12862, A
c 9	278.8	20.7	601	4	US-09-949-016-20240	Sequence 20240, A
c 10	278.8	20.7	601	4	US-09-949-016-42446	Sequence 42446, A
11	177.6	13.3	2079	4	US-09-949-016-3691	Sequence 3691, Ap
12	177.6	13.2	2768	4	US-09-949-016-1221	Sequence 1221, Ap
13	163.6	12.2	2059	4	US-09-023-655-1062	Sequence 1062, Ap
14	153.	11.4	2080	4	US-09-949-016-3690	Sequence 3690, Ap
15	135.6	10.1	2759	3	US-09-144-367-1	Sequence 1, Appli
c 16	124.4	9.2	601	4	US-09-949-016-93499	Sequence 93499, A
17	119	8.8	1707	4	US-09-023-655-1060	Sequence 1060, Ap
18	119	8.8	1707	4	US-09-949-016-121	Sequence 121, App
19	119	8.8	1707	4	US-09-949-016-1220	Sequence 1220, Ap
20	115.8	8.6	1659	4	US-09-583-447A-1	Sequence 1, Appli
21	107.4	8.0	1599	4	US-09-023-655-1405	Sequence 1405, Ap
22	106	7.9	106	4	US-09-583-447A-39	Sequence 39, Appl
23	88.4	6.6	106	4	US-09-583-447A-40	Sequence 40, Appl
24	74.6	5.5	106	4	US-09-583-447A-41	Sequence 41, Appl
25	73.6	5.5	1512	4	US-08-277-031B-4	Sequence 4, Appli
c 26	70	5.2	7218	1	US-08-233-463-14	Sequence 14, Appl
27	66	4.9	106	4	US-09-583-447A-42	Sequence 42, Appl

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:12:33 ; Search time 1335.47 Seconds  
(without alignments)  
5961.965 Million cell updates/sec

Title: US-09-943-115A-1

Perfect score: 1345

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2002bs:\*
- 8: Geneseq2003as:\*
- 9: Geneseq2003bs:\*
- 10: Geneseq2003cs:\*
- 11: Geneseq2003ds:\*
- 12: Geneseq2004as:\*
- 13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1344.2	99.9	1345	2	Aax28296 Human CYP
2	1344.2	99.9	1345	3	Aaz57019 Nucleic a
3	1344.2	99.9	1345	3	Aaz57020 Nucleic a
4	1344.2	99.9	1345	6	Abk68745 5'-flanki
5	1344.2	99.9	1345	12	AdJ84441 Human phe
6	1310	97.4	6101	13	AdS89077 Human CYP
7	1310	97.4	96960	8	AcF62734 Cancer ba
8	1310	97.4	96960	8	AdB20849 MRP1 base
9	1310	97.4	96960	10	AdB87938 Human UGT
10	1310	97.4	96960	10	AdB96921 Human CYP
11	1310	97.4	96960	10	AdB92112 Human MDR
12	1310	97.4	123785	10	AdB77171 DNA seque
13	1305.2	97.0	39071	12	AdM97420 Prostata
14	1190.2	88.5	13035	8	AdS51997 Human CYP
15	1153.2	85.7	15185	8	AdS2000 Human CYP
16	1140.2	84.8	12983	6	AdA41239 Human CYP
17	924.4	68.7	11186	6	AdA41242 Human CYP
18	924.4	68.7	11186	6	AdA36213 Human CYP
19	817.6	60.8	6101	13	AdS89415 Human CYP
20	814.4	60.6	6101	13	AdS89689 Oligonuclei

21	813.2	60.5	1012	6	AdA36215 Human pro
22	746.8	55.5	6101	13	AdS89416 Oligonuclei
23	743.6	55.3	6101	13	AdS89690 Oligonuclei
24	646.4	48.1	8943	6	AbK39966 Human che
25	578.8	43.0	8943	6	AbK39967 Human che
26	518.4	38.5	36902	6	AdA43350 Human cyt
27	518.4	38.5	177531	8	AcF62732 Cancer ba
28	518.4	38.5	177531	8	AdB20847 MRP1 base
29	518.4	38.5	177531	10	AdS87936 Human UGT
30	518.4	38.5	177531	10	AdB96919 Human MDR
31	518.4	38.5	177531	10	AdB92112 Human MDR
32	518.4	38.5	177531	10	AdH74617 Human BAC
33	483.4	35.9	830	6	AbK99500 Human CYP
34	481.8	35.8	830	6	AbK99410 Human CYP
35	481.8	35.8	830	6	AbK99409 Human CYP
36	481.8	35.8	830	6	AbK99524 Human CYP
37	480.2	35.7	830	6	AbK99501 Human CYP
38	480.2	35.7	830	6	AbK99411 Human CYP
39	480.2	35.7	830	6	AbK99412 Human CYP
40	480.2	35.7	830	6	AbK99412 Human CYP
41	458.2	34.1	1001	13	AdQ81033 Human phe
42	438.4	32.6	1346	3	AAA51756 Cytochrom
43	309.6	23.0	8776	6	AbK40067 Human che
44	291	21.6	1365	13	ACN41767 Human dia
45	291	21.6	2041	13	ACN41766 Human dia

#### ALIGNMENTS

#### RESULT 1

AAx28296  
ID AAx28296 standard; DNA; 1345 BP.

XX  
AC AAx28296;

XX  
DT 17-JUN-1999 (first entry)

XX  
DE Human CYP3A4 gene promoter.

XX  
KW CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;  
KW CYP3A4 substrate; drug-drug interaction identification; toxin exposure;  
KW genetic linkage detection; phenotypic variation; promoter; ss.

XX  
OS Homo sapiens.

XX  
PN WO9913106-A1.

XX  
PD 18-MAR-1999.

XX  
PF 02-SEP-1998; 98WO-US018158.

XX  
PR 10-SEP-1997; 97US-0058612P.

XX  
PA (AXYS-) AXYS PHARM INC.

XX  
PI Lichter JB, Guida M;

XX  
DR WPI, 1999-215070/18.

XX  
PT New isolated CYP3A4 polymorphic sequences.

XX  
PS Disclosure; Page 29; 40pp; English.

CC This sequence represents the human CYP3A4 gene promoter. The invention relates to a CYP3A4 sequence polymorphism, which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYP3A4 polymorphic sequences can be used to screen patients for altered metabolism for CYP3A4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establish animal, cell culture and in vitro cell-free models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used for expression studies to

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1344.2	99.9	1345	6	AR142139	Sequence
2	1344.2	99.9	1345	6	AR142140	Sequence
3	1344.2	99.9	1345	6	BD222974	CYP2A4 NF
4	1344.2	99.9	1345	6	BD222975	CYP2A4 NF
5	1344.2	99.9	1345	6	CQ776018	Sequence
6	1344.2	99.9	1345	6	CQ790615	Sequence
7	1344.2	99.9	1345	6	AR222893	Sequence
8	1344.2	99.9	1345	6	AX421253	Sequence
9	1344.2	99.9	1345	6	HUMCYF3A4	Sequence
10	1310	97.4	6101	6	CQ806643	Sequence
11	1310	97.4	96960	6	AX706964	Sequence
12	1310	97.4	96960	6	AX707894	Sequence
13	1310	97.4	123778	9	AC069294	Sequence
14	1310	97.4	174832	9	AF280107	Homo sapi
15	1308.4	97.3	11374	9	AF185589	Homo sapi
16	1244.6	92.5	170470	9	AF1846392	Homo sapi
17	1101.4	81.9	183854	2	AC146392	Pan trogl
18	1101.2	81.9	173861	2	AC145951	Pan trogl
19	993.8	73.9	1013	9	AF181105	Homo sapi